AMENDMENT TO THE CLAIMS:

This listing of claims will replace all prior listings of claims in the application:

LISTING OF CLAIMS:

Claims 1-234 were cancelled in an Amendment dated January 11, 2005.

Claims 235-286 are cancelled herein.

287. (Previously Presented) A method for identifying a compound that putatively elicits or modulates taste in a human subject based on its effect on the activation of a taste receptor comprising a human T1R2 polypeptide comprising:

(i) screening one or more compounds in a functional assay that detects compounds which activate or modulate (enhance or inhibit) the activation of a taste receptor comprising a human T1R2 polypeptide selected from the group consisting of:

(a) a human TlR2 polypeptide having the amino acid sequence in SEQ. ID. NO: 21;

(b) a human T1R2 polypeptide that possesses at least 90% sequence identity to the polypeptide in SEQ. ID. NO: 21;

(c) a human T1R2 polypeptide which encoded by a nucleic acid sequence that hybridizes to the T1R2 polypeptide coding region of the nucleic acid sequence in SEQ. ID. NO: 23 under stringent hybridization conditions which are incubation in 50% formamide, 5X SSC and 0.1% SDS, with wash in 0.2X SSC and 0.1% SDS at 65 degrees C and which taste receptor comprising said human T1R2 polypeptide specifically binds to a ligand that also specifically binds to the human T1R2 polypeptide in SEQ ID NO:21;

(ii) identifying compounds (i) that putatively elicit or modulate T1R2 polypeptide-associated taste subject based on their (a) activation or modulation (inhibition or enhancement) of the activation of said T1R2 polypeptide according to (a), (b), or (c), in said functional assay (i).

288. (Previously Presented) The method of claim 287, wherein said T1R2 polypeptide has the amino acid sequence in SEQ. ID. NO: 21.

289. (Previously Presented) The method of claim 287, wherein said T1R2 polypeptide has an amino acid sequence that possesses at least 90% sequence identity to the polypeptide in SEQ. ID. NO: 21.

290. (Previously Presented) The method of claim 287, wherein said T1R2 polypeptide has an amino acid sequence that possesses at least 95% sequence identity to the polypeptide in SEQ. ID. NO: 21.

291. (Previously Presented) The method of claim 287, wherein said T1R2 polypeptide has an amino acid sequence that possesses at least 96% sequence identity to the polypeptide in SEQ. ID. NO: 21.

292. (Previously Presented) The method of claim 287, wherein the T1R2 polypeptide possesses at least 97% sequence identity to the polypeptide in SEQ. ID. NO: 21.

293. (Previously Presented) The method of claim 287, wherein said T1R2 polypeptide has an amino acid sequence that possesses at least 97% sequence identity to the polypeptide in SEQ. ID. NO: 21.

294. (Previously Presented) The method of claim 287, wherein said TlR2 polypeptide has an amino acid sequence that possesses at least 98% sequence identity to the polypeptide in SEQ. ID. NO: 21.

295. (Previously Presented) The method of claim 287, wherein said T1R2 polypeptide has an amino acid sequence that possesses at least 99% sequence identity to the polypeptide in SEQ. ID. NO: 21.

296. (Previously Presented) The method of claim 287, wherein said T1R2 polypeptide is encoded by a nucleic acid sequence that hybridizes to the T1R2 coding region in SEQ. ID. NO: 23 under stringent hybridization conditions.

297. (Previously Presented) The method of claim 287, wherein said T1R2 polypeptide is expressed in a cell.

298. (Previously Presented) The method of claim 297, wherein said cell is intact or permeabilized.

299. (Previously Presented) The method of claim 287, wherein said T1R2 polypeptide is comprised in a membrane extract.

300. (Previously Presented) The method of claim 297, wherein said T1R2 polypeptide is expressed on the surface of said cell.

301. (Previously Presented) The method of claim 297, wherein the cell is a prokaryotic cell.

302. (Previously Presented) The method of claim 297, wherein the cell is a eukaryotic cell.

303. (Previously Presented) The method of claim 302, wherein said cell is a yeast, insect, amphibian or mammalian cell.

304. (Previously Presented) The method of claim 302, wherein the cell is a CHO, HEK-293, COS or Xenopus oocyte.

305. (Previously Presented) The method of claims 296, wherein said cell expresses a G protein.

306. (Previously Presented) The method of claim 305, wherein said G protein is $G_{\alpha 15}$ or $G_{\alpha 16}$ or gustducin.

307. (Previously Presented) The method of claim 287, wherein said functional assay detects the effect of said compound on phosphorylation of the TlR2 polypeptide.

308. (Previously Presented) The method of claim 287, wherein the functional assay detects the effect of said compound on the dissociation of said TlR2 polypeptide and a G protein.

309. (Previously Presented) The method of claim 287, wherein the functional assay detects the effect of said compound on arrestin translocation.

310. (Previously Presented) The method of claim 287, wherein the functional assay detects the effect of said compound on second messenger(s).

311. (Previously Presented) The method of claim 287, wherein the functional assay detects the effect of said compound on signal transduction.

312. (Previously Presented) The method of claim 287, wherein the functional assay is a fluorescent polarization assay.

313. (Previously Presented) The method of claim 311, wherein said functional assay is a GTPγ^{35}S assay.

314. (Previously Presented) The method of claim 311, wherein said functional assay detects changes in cAMP, cGMP or IP3.

315. (Previously Presented) The method of claims 287, wherein said functional assay detects changes in intracellular calcium.

316. (Previously Presented) The method of claim 315, which uses a calcium-sensitive dye.

317. (Previously Presented) The method of claim 287 which detects the effect of said compound on G protein activation by said T1R2 polypeptide.

318. (Previously Presented) The method of claim 317, wherein said G protein is $G_{\alpha 15}$, $G_{\alpha 16}$ or gustducin.

319. (Previously Presented) The method of claim 287, wherein said T1R2 polypeptide in said functional assay is stably or transiently expressed by a cell.

320. (Previously Presented) The method of claim 287, wherein the functional assay detects changes in ionic polarization of a cell or membrane that expresses the T1R2 polypeptide.

321. (Previously Presented) The method of claim 320, wherein ion polarization is detected by a voltage-clamp or patch-clamp method.

322. (Previously Presented) The method of claim 287, wherein said functional assay comprises a radiolabeled ion flux assay or fluorescence assay that detects T1R2 activity using a voltage-sensitive dye.

323. (Previously Presented) The method if claim 287, wherein said assay comprises a fluorescent polarization or FRET assay.

324. (Previously Presented) The method of claim 287, wherein said assay detects changes in adenylate cyclase activity.

325. (Previously Presented) The method of claim 287 wherein the functional assay detects changes in ligand-dependent coupling of said T1R2 polypeptide with a G protein.

326. (Previously Presented) The method of claim 325, wherein said G protein is $G_{\alpha 15}$ or $G_{\alpha 16}$ or gustducin.

327. (Previously Presented) The method of claim 287, wherein said functional assay detects changes in intracellular cAMP or cGMP.

328. (Previously Presented) The method of claim 287, wherein said assay measures the effect of said compound on transmitter or hormone release.

329. (Previously Presented) The method of claim 287 wherein said functional assay detects the effect of said compound on the transcription of a gene of interest.

330. (Previously Presented) The method of claim 329, wherein said gene is a reporter selected from chloramphenicol acetyltransferase, luciferase, 3'-galactosidase and alkaline phosphatase.

331. (Previously Presented) The method of claim 287, wherein the functional assay is a high throughput assay.

332. (Previously Presented) The method of 331, wherein said functional assay screens a library of compounds.

333. (Previously Presented) The method of claim 332 wherein said library is a combinatorial chemical library.

334. (Previously Presented) The method of claim 332 wherein said library comprises at least 1000 compounds.

335. (Previously Presented) The method of claim 287, wherein the effect of said putative T1R2 taste modulator is assayed in vivo for its effect on T1R2 receptor polypeptide-associated taste.

336. (Previously Presented) The method of claim 335 which is used to assay the effect of said compound on the taste of a particular compound.

337. (Previously Presented) The method of claim 336, wherein said assay is used to detect the effect of said compound on sweet or umami taste.

338. (New) The method of claim 287 wherein said human T1R2 polypeptide is expressed by a taste cell , gastriointestinal cell. geschmackstreifen, oral cavity, or epiglottis cell.

339. (New) The method of claim 287 wherein said T1R2 polypeptide is expressed by a gastroepithelial cell, esophageal cell, stomach cell or cell derived from the palate.

340. (New) The method of claim 338 wherein the taste cell is a foliate, fungiform, or circumvallate cell..